Listing of Claims:

This listing of claims will replace all prior versions and listings of the claims in this application.

1.   (Previously presented) A method of estimating a genetic relationship between a poinsettia plant and a known poinsettia cultivar, the method comprising the steps of:

(a)   obtaining a DNA fingerprint of the poinsettia plant's genomic DNA by AFLP, the fingerprint comprising a collection of amplified polymorphic restriction fragments;

(b)   comparing the fingerprint obtained in (a) with a genomic DNA fingerprint of the known poinsettia cultivar; and

(c)   estimating the genetic relationship between the plant and the cultivar by determining the degree of similarity between the fingerprints.

2.   (Previously presented) The method of Claim 1, wherein the amplified polymorphic restriction fragments comprise DNA sequences that include DNA sequences **SEQ ID NOS**: **12, 20, 21, 22, 23, 24, 34, 35,** and **37.**

3.   (Previously presented) A method of assessing the breeding history of a first poinsettia plant, comprising:

(a)   obtaining a DNA fingerprint of the genomic DNA of a first poinsettia plant by AFLP, wherein the fingerprint comprises a set of amplified polymorphic restriction fragments;

(b)   comparing the fingerprint of the first poinsettia plant with a fingerprint of the genomic DNA of a poinsettia plant that is a representative member of a specific breeding family, wherein the fingerprint comprises a set of amplified polymorphic restriction fragments; and

(c)   generating a profile index value based on the comparison of the fingerprint of the first poinsettia plant with the fingerprint of the poinsettia plant that is a representative member of a specific breeding family, thereby assessing the breeding history of a poinsettia plant.

4.   (Previously presented) The method of Claim 3, wherein the amplified polymorphic restriction fragments comprise DNA sequences that include DNA sequences **SEQ ID NOS**: **12, 20, 21, 22, 23, 24, 34, 35,** and **37**.

5.   (Previously presented) The method of Claim 3, wherein the specific breeding family is selected from the group consisting of the Freedom, Peterstar, and Sonora breeding family.

6.   (Original) The method according to Claim 3, wherein the AFLP analysis is carried out by first digesting the genomic DNA with a restriction enzyme that has a tetranucleotide recognition site and a restriction enzyme that has a hexanucleotide recognition site.

7.   (Original) The method according to Claim 6, wherein the restriction enzyme that has a tetranucleotide recognition site is *Mse*I, and the restriction enzyme that has a hexanucleotide recognition site is *Eco*RI.

8-9   (Canceled).

10.   (Previously presented) The method of Claim 3, wherein the fingerprint of the genomic DNA of the first poinsettia plant is used to generate a profile of the poinsettia plant, wherein the profile comprises the set of amplified polymorphic restriction fragments that comprise DNA sequences that include the DNA sequences **SEQ ID NOS**: **12, 20, 21, 22, 23, 24, 34, 35,** and **37**; and wherein (b) comprises comparing the profile of the poinsettia plant to a profile generated from the fingerprint of the poinsettia plant that is a representative member of a specific breeding family, wherein the profile of the poinsettia plant that is a representative member of a specific breeding family comprises the set of amplified polymorphic restriction fragments that comprise DNA sequences that include the DNA sequences **SEQ ID NOS**: **12, 20, 21, 22, 23, 24, 34, 35** and **37**.

11.   (Previously presented) The method of Claim 10, wherein the profile of at least one of the first poinsettia plant and the profile of the poinsettia plant that is a representative member of a specific breeding family is stored in a database comprising profiles of known poinsettia cultivars, and wherein the profiles of the known poinsettia cultivars comprise the set of amplified polymorphic restriction fragments that comprise DNA sequences that include the DNA sequences **SEQ ID NOS: 12, 20, 21, 22, 23, 24, 34, 35,** and **37.**

12-20 (Canceled).

21.   (Previously presented) A method of determining the profile similarity of a first poinsettia plant to a second poinsettia plant, comprising:

(a)   obtaining a DNA fingerprint of the genomic DNA of a first poinsettia plant by AFLP, wherein the fingerprint comprises a set of amplified polymorphic restriction fragments;

(b)   comparing the fingerprint of the first poinsettia plant with a fingerprint of the genomic DNA of the second poinsettia plant, wherein the fingerprint comprises a set of amplified polymorphic restriction fragments; and

(c)   generating a profile index value based on the comparison of the fingerprint of the first poinsettia plant with the fingerprint of the second poinsettia plant, thereby estimating the profile similarity of the first poinsettia plant to the second poinsettia plant.

22.   (Previously presented) The method according to Claim 21, wherein the amplified polymorphic restriction fragments comprise DNA sequences that include DNA sequences **SEQ ID NOS: 12, 20, 21, 22, 23, 24, 34, 35,** and **37.**

23.   (Original) The method according to Claim 21, wherein the AFLP analysis is carried out by first digesting the genomic DNA with a restriction enzyme that has a tetranucleotide recognition site and a restriction enzyme that has a hexanucleotide recognition site.

24.   (Original) The method according to Claim 23, wherein the restriction enzyme that has a tetranucleotide recognition site is *Mse*I, and the restriction enzyme that has a hexanucleotide recognition site is *Eco*RI.

25-26 (Canceled).

27.   (Previously presented) The method of Claim 21, wherein the fingerprint of the genomic DNA of the first poinsettia plant is used to generate a profile of the poinsettia plant, wherein the profile comprises the set of amplified polymorphic restriction fragments that comprise DNA sequences that include the DNA sequences **SEQ ID NOS: 12, 20, 21, 22, 23, 24, 34, 35, and 37**; and wherein (b) comprises comparing the profile of the poinsettia plant to a profile generated from the fingerprint of the second poinsettia plant, wherein the profile of the second poinsettia plant comprises the set of amplified polymorphic restriction fragments that comprise DNA sequences that include the DNA sequences **SEQ ID NOS: 12, 20, 21, 22, 23, 24, 34, 35, and 37**.

28.   (Previously presented) The method of Claim 27, wherein the profile of at least one of the first and the second poinsettia plants is stored in a database comprising profiles of known poinsettia cultivars, and wherein the profiles of the known poinsettia cultivars comprise the set of amplified polymorphic restriction fragments that comprise the DNA sequences **SEQ ID NOS: 12, 20, 21, 22, 23, 24, 34, 35, and 37**.

29.   (Original) The method according to Claim 28, wherein the database is stored in a computer-readable storage medium.

30.   (Original) The method according to Claim 21, wherein the comparing step is carried out by a computer.

31-51 (Canceled).

52.   (Previously presented) The method of claim 64, wherein the comparison between the profile of the poinsettia plant and the known poinsettia cultivar is carried out by a computer.

53-62 (Canceled).

63.   (Previously amended) A method of determining whether a poinsettia plant is a representative of a known poinsettia cultivar, comprising:

(a)   obtaining a DNA fingerprint of the genomic DNA of a poinsettia plant by AFLP analysis; and

(b)   comparing the fingerprint of (a) with a fingerprint of the genomic DNA of the known poinsettia cultivar;

wherein the poinsettia plant is a representative of the known poinsettia cultivar if the fingerprint of the poinsettia plant and the fingerprint of the known poinsettia cultivar have the same complement of polymorphic bands.

64.   (Previously presented) The method according to Claim 63, wherein the DNA fingerprint of the genomic DNA is a set of amplified polymorphic restriction fragments, and wherein the amplified polymorphic restriction fragments comprise DNA sequences that include DNA sequences **SEQ ID NOS: 12, 20, 21, 22, 23, 24, 34, 35,** and **37**.

65-68 (Canceled).

69.   (Previously presented) A method of distinguishing a poinsettia cultivar from a known poinsettia cultivar, comprising:

obtaining a DNA fingerprint of the genomic DNA of a poinsettia plant by AFLP analysis and;

comparing the fingerprint of (a) with a fingerprint of the genomic DNA of the known poinsettia cultivar;

wherein the poinsettia plant is not a representative of the known poinsettia cultivar if the fingerprint of the poinsettia plant and the fingerprint of the known poinsettia cultivar are not essentially the same.

70-74. (Canceled).